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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 158.91 Seconds 861.291 Million cell updates/sec Fri May 14 08:07:02 1999; :uo

n.a. database search, using Smith-Waterman algorithm

n.a.

MPsrch_nn

>US-08-911-423-3 (1-1006) from US08911423.seq 1006 not generated. ular output Description: Perfect Score: Title:

1 ATGGCACAGCAGCAGCGGT......ACAACGTCCTGACTGGGAAA 1006 TACCGTGTCGTGCCCCGGTA......TGTTGCAGGACTGACCCTTT Sequence: N.A.

Scoring table:

TABLE default Gap 6

STD

Nmatch

188442 segs, 68026449 bases x 2 Dbase 0; Query 0 Searched:

Minimum Match 08 Listing first 45 summaries Post-processing:

n-geneseq32 Database:

| Spart | 2.part | 3.part | 4.part | 5.part | 5.part | 7.part | 5.part | 2.part | 2.part | 2.part | 2.part | 2.part | 2.part | 3.part | 10.part | 11.part | 11.part | 13.part |

Mean 8.892; Variance 5.749; scale 1.547

istics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						COLUMNICO		
			оф					
Res	Result No.	Score	Query Match	Query Match Length DB	DB	11	Description	Pred. No.
•	:				1			
υ	1	114	11.3	3327	30	T69936	Coprinus cinereus lac	1.47e-52
	7	96	9.5	2606	14	083527	P. falciparum E31a de	2.05e-41
	٣	96	9.5	2606	32	T72895	Plasmodium E31a gene.	2.05e-41
	4	85	8.4	1581	22	T32233	Cuphea C14:0-ACP thio	1.08e-34
	Ŋ	71	7.1	533	38	V02890	Human HMGI-C aberrant	2.80e-26
	9	65	6.5	774	38	V02883	Human HMGI-C aberrant	9.86e-23
	7	59	5.9	797	38	V02898	Human HMGI-C aberrant	3.12e-19
	œ	43	4.3	91	σ	051746	Oligonucleotide probe	3.27e-10
υ	σ	42	4.2	91	σ	051746	Oligonucleotide probe	1.14e-09
υ	10	42	4.2	204	ч	N81164	Base substituted E.co	1.146-09
	11	41	4.1	178	32	T76405	Human endothelin-1 an	3.97e-09
	12	39	9.8	204	П	N81164	Base substituted E.co	4.69e-08
U	13	39	3.9	206	23	T27694	pGEM32f target fragme	4.69e-08

1	4.69e-08	.69e-	4.69e-08	•	4.69e-08	4.69e-08	•	4.69e-08	9.	4.69e-08	4.69e-08	4.69e-08	'n	4.69e-08	4.69e-08	4.69e-08	4.69e-08	4.69e-08	•	4.69e-08	4.69e-08	4.69e-08	4.69e-08	•	•	4.69e-08	4.69e-08	4.69e-08	•	0-96	- Эе-	4.69e-08
	DNA substrate for 5'	5' Nuclease substrate	Human TSH beta-chain	Polynucleotide encodi	Sequence from phage M		T. hyo gene 6:lacZ fu	Expression cassette c		I2C-4 gene encoding F		_	Plasmid pKSEL5.	Plasmid pBSGFP expres		çţ	Plasmid pAT-1 sequenc	of plasmi	l gr	꼇	Plasmid pinvi.	Human type C lectin e	Plasmid GS contg. N.		Plasmid glucoamylase	ŝ	Plasmid pWRG3169 enco	Intron 21 of human pR	irus vector		pM16.	Retro virus vector p5
		080775	T27571	T99561	N40087	N50326.	011381	971364	971365	T42137	T92869	V03313	013578	V14340	T69189	T69188	T04575	054144	T86610	T86449	087347	V02186	084696	T04569	084694	039020	V02042	T96851	3	081226	2	073735
	37	13	23	40	က	m	~	12	12	25	38	40	~	39	35	35	16	σ	37	35	14	38	15	16	15	ဖ	39	38		20		12
	206	228	349	696	1287	1287	1380	1619	1754	2027	3198	3212	3681	3699	4118	4118	4164	4274	4283	4283	4539	4771	4792	93	5042	6824	7287	9837	10306	10930	10950	10970
				•															•												3.9	٠.
	39	36	39	39	39	39	39	39	39	39	39	39	39	39	33	39	33	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38		40		42	43	44	45
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ALIGNMENTS

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Coprinus cinereus laccase loc1 genomic DNA.

Benzenediol.oxygen oxidoreductase; laccase; lignin; Kraft pulp; dye; fungus; polymerase chain reaction; papermaking; ss.

Coprinus cinereus (strain IFO 8371).

Key 1.851

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                                                                                                                                                                  /cons_splice= (5'site:YES,3'site:YES)
/note= "The printed version of the sequence has the following splice junction sequences (with exon nucleotides shown in capitals and intron nucleotides shown in lower case):
5' site:GC/gt and 3' site:ag/TG"
                                                                                                                                                                                                                                                                                                                                                                                /cons_splice= (5'site:NO,3'site:NO)
/note= "The printed version of the sequence has the
                                                                                                                                                                                                                                                                                                     /cons_splice= (5'site:YES,3'site:YES)
1101..1248
                                                                                                                              /codon_start= 726
852..906
           BP.
                                                                                                                                                    /*tag= b
/number= 1
 T 1
T69936 standard; DNA; 3327
                                                                                                                                                                                                                                                             /number= 2
1024..1100
                                                                                                                                                                                                                                                                                                                                      /number= 3
1249..1316
                                (first entry)
                                                                                                                                                                                                                                                    /*tag= c
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                                                                                                                                                                                                                                                                                             /number=
                                                                                                                                                                                                                                                                                                                                                                      /number=
                     T69936;
21-JUL-1997
                                                                                                                                         intron
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                                                                                                                                                                                                                                          exon
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RESULT
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The present sequence encodes a novel laccase, lccl, isolated from the present sequence encodes a novel laccase, lccl, isolated from Coprinus cinercus strain IFO 8371. This polypeptide is used to polymerise a lignin or lignosulphate in solution; for in situ depolymentsation of Kraft pulp; for oxidising dyes or their precursors of particularly to prevent dye transfer between fabrics and in hair dyeing) and for polymerising or oxidising phenolic compounds (e.g. to precipitate phenolics from fruit juices to give a more stable product). It can also be used for soil detoxification. Use of the polypeptide avoids the need to use chlorine for lignin depolymerisation. It has better activity than known laccases under the alkaline conditions usually encountered in papermaking processes. A CDNA library from
                                                                                                                                                            /cons_splice= (5'site:NO,3'site:NO)
/note= "The printed version of the sequence has the following splice junction sequences (with secon nucleotides shown in capitals and intron nucleotides shown in lower case):
5' site:TG/gt and 3' site:ag/gr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  / number = 6
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// number = 6
// cons_splice = (5'site:YES,3'site:YES)
// note = "The printed version of the sequence has the following splice junction sequences (with exon nucleotides shown in capitals and intron nucleotides shown in lower case):
5. site:AM/qt and 3' site:ag/CG"
2548..2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New laccase from Coprinus strains - useful for polymerising lignin, depolymerising Kraft pulp, oxidising dyes and their precursors, etc. Claim 18; Fig 1; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note- "The printed version of the sequence has the
following splice junction sequences (with exon nucleotides shown in capitals and intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                following splice junction sequences (with exon nucleotides shown in capitals and intron
                                                                                                                                                                                                                                                                                                              /number= 5
/cons.splice= (5'site:YES,3'site:YES)
2321..2494
/*tag* k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cons_splice= (5'site:NO,3'site:NO)
                                 nucleotides shown in lower case):
5' site:TG/gt and 3' site:ag/GC"
1317..1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotides shown in lower case)
5' site:TG/gt and 3' site:ag/TC"
5/511..3327
/*tag= o
/number= 8
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P-PSDB; W17973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-1995; US-002800.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
                                                                                                             1698..1752
/*tag= h
                                                                                                'number= 4
                                                                                                                                                                                                                                                            1753..2240
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                                                                                                                                                                                                                                                                                                                                                                                                          'number= 6
                                                                                                                                                /number= 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9708325-A2
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based on the conserved motifs in other fungal laccases. The based on the conserved motifs in other fungal laccases. The amplification product was cloned and 7 subclues were produced and sequenced. They correspond to 3 different laccases designated loc1, 2 and 3. To isolate full-length DNA, a genomic DNA library of IFO 8371 was constructed. A digoxigenin-labelled probes from loc2 and 3 partial cDNA. These probes were used to screen the genomic library and two clones were isolated, one containing the loc1 gene and the other containing the loc3 gene. No single clone contained the complete loc2 gene which was isolated from two partial clones.

N.B. The sequence presented in this record is the same as the version supplied electronically to the Buropean Patent Office; it differs from the sequence printed in Figure 1 of the specification at some of the exon/intron boundaries. See features table.

Sequence 3327 BP; 770 A; 917 C; 811 G; 829 T;
                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 tttcccagtcacgacgttgtaaaacgacggccagtgaattgaatttaggtgacactatag 461
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          083527;
22-SEP-1995 (first entry)
P. falciparum E31a gene.
Erythrocyte binding ligand, E31a; binding domain; malaria; therapy; vaccine; ss.
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 51-52, 81pp; English.

Erythrocyte binding ligand (EBL) family genes were cloned from P. falciparum chromosome 7 subsegment libraries constructed during genetic studies of the chloroquine resistance locus. The 4 genes, EBL-e1 (083526), EBL-e2 (083528) and Proj3 (083529), encode the proteins given in R70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, mammalian, insect, and in vaccinia virus and adenovirus-infected cells, and provide protection against P. falciparum. Sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New erythrocyte binding domain polypeptide(s) - isolated from Plasmodium binding proteins, used in diagnosis, treatment and prevention of malaria
                                                                                                                                                                                                                                                                                                                            Length 3327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 2606;
                                                                                                                                                                                                                                                                                                                          Score 114; DB 30; Length 33
Pred. No. 1.47e-52;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Su X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.05e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1994; U10230.

10-SEP-1993; US-119677.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Chitnis C, Miller LH, Peterson DS, Sim KL,
Wellems TE;
WPI; 95-123427/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%; Score 96; 99.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 2
Q83527 standard; DNA; 2606 BP.
                                                                                                                                                                                                                                                                                                                          Match 11.3%;
Local Similarity 97.5%;
Les 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 99.0%;
les 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9507353-A.
16-MAR-1995.
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
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949 ATAGIGICACCIAAATICAATICACIG 975
                                                                                                                                                                                                       Voelker TA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HMGI-C aberrant form 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1997.
21-DEC-1995; 048122.
21-DEC-1995; DE-048122.
                                                                                                               02-FEB-1995; US-383756.
05-JUN-1995; US-460898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue regeneration; ss
                                                                                                                                                                                  wellsh K, Hawkins D, wpl; 96-371439/37.
P-PSDB; W02081.
/*tag=
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                                                                                                                                                                      (CALJ ) CALGENE INC
Dehesh K, Hawkins I
                                                                              01-FEB-1996; U01585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
DE19548122-A1.
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V02890
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This sequence represents the Elaa gene of Plasmodium. Ella belongs to the Duffy binding proteins

This sequence represents the Elaa gene of Plasmodium. Ella belongs to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see 172889 and 772888 respectively). The var family of genes modulate cytoadherence and antigenci variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein that appear in the culture protein (DABP) are soluble proteins that appear in the culture conservation of merozoites release merozoites. DABP and SABP conservation of merozoites release merozoites. DABP and SABP conservation of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the compositions are for the treatment and prevention of malaria, and compositions are for the treatment and prevention of malaria, and compositions are used for the treatment and prevention of malaria. They compositions are used for the treatment and prevention of malaria. They compositions are used for the treatment and prevention of malaria. They compositions are used for the treatment and prevention of malaria. They care also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caagettacgtacgegtgcatgcgacgtcatagetettetatagtgtcacctaaattcaa 2514
                                                                                                                                     Plasmodium E31a gene.

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;

Duffy binding like gene: Duffy antigen binding protein; erythrocyte;

DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        909 CAAGCITACGTACGCGTGCATGCGACGTCATAGCTCTTTATAGTGTCACCTAAATTCAA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 32; Length 2606;
Pred. No. 2.05e-41;
0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1996 (first entry)
Cuphea C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2).
Whylistate; myristic acid; fatty acid; acyl-ACP thioesterase;
Myristate; myristic acid; fatty acid; acyl-ACP thioesterase;
seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "encodes residues 1-785 of W22480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Su x;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996; U09508.
07-JUN-1995; US-487826.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                     .T 3
T72895 standard; cDNA; 2606 BP.
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Local Similarity 99.0%;
les 97; Conservative
                                                                                                            07-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                     106..2460
                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-052231/05.
P-PSDB; W22480.
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                                                                                                                                                                                                                                                              Plasmodium; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chitnis C,
Wellems TE
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                                                                              T72895
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kits can reduce, block or stimulate angiogenesis or vascularisation and can improve vascular provision in myocardium damaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The regeneration method can be applied to tissues which are currently impossible or difficult to regenerate and the use of blological material with attendant risks of viral transmission and anaphylactic shock, is avoided.
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Recombinant produ. of myristate in plant cells - using DNA with preferential activity on C14 fatty acids from Cuphea palustris, nutmeg and camphor, useful in detergent and food industries.

Example 1: Fig 1A-1E: 77pp: Bradish.

C A CDNA Clone (T32233), designated MCT34 (pCpFatE2), codes for Cuphea palustris C14:0-ACP thioesterase (W02081), an enzyme that acts primarily on C14:0-ACP substrates, forming C14:0 (myristate). It was isolated from a developing seed CDNA library by screening with sequences encoding medium-chain acyl-ACP thioesterases from Cuphea hookeriana. Constructs for expression of clone MCT34 in plant seeds under the control of napin or oleosin regulatory regions were prepd. These allow high-level prodn. of myristate (useful in surfactants and foods) in plant cells, e-g. Brassica.

Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bullerdisk J;
WRI: 97-333837/31.
DNA sequences representing aberrant forms of human high mobility group protein genes - useful for treatment of endometriosis and tumours, or for modulating vascularisation, etc
Lumours, or for modulating vascularisation, etc
Lumin 1: Fig 11: S8Pp; German.
V02880-V02898 are CDNA sequences that encode aberrant forms of the human high mobility group protein (HMG) gene, HMGI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein binding domain. These proteins antibodies derived from these proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascular development. Suc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High mobility group protein; HMGI-C; MAG; human; treatment; modulator; multiple tumour aberration growth gene; vascular development; anglogenesis; vascularisation; endometriosis; contraception
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8.4%; Score 85; DB 22; Length 1581;
Best Local Similarity 98.9%; Pred. No. 1.08e-34;
Matches 86; Conservative 0: Mismatches 1. Tadale (
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high mobility group procein (RMG) gene, HMGI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein binding domain. These proteins, antibodies derived from these proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascular development. Such kits can reduce, block or stimulate angiogenesis or vascularisation and can improve vascular provision in myocardium damaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The regeneration method can be applied to tissues which are currently impossible or difficult to regenerate and the use of biological material with attendant risks of viral transmission and
                                                                                                                                                           WPI; 97-333837/31.

DNA sequences representing aberrant forms of human high mobility group protein genes - useful for treatment of endometriosis and tumours, or for modulating vascularisation, etc claim 1; Fig 19; 58pp; German.

V02880-V02898 are cDNA sequences that encode aberrant forms of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          735 ggcggccgctctagaggatccaagcttacgtacgtggcatgcgacgtcatagctcgtct 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 38; Leuy...
Pred. No. 3.12e-19;
....matrhes 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c shock, is avoided.
797 BP; 267 A;
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
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Local Similarity 96.8%;
nes 61; Conservative
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    regeneration; ss.
                                                          26-JUN-1997.
21-DEC-1995; 048122.
21-DEC-1995; DE-048122.
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                                                                                                                         (BULL/) BULLERDIEK J.
                       Homo sapiens.
DE19548122-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumours, or for modulating vascularisation, etc. Claim 1: Fig 4: 58pp; German.
V02880-V02898 are cDNA sequences that encode aberrant forms of the human high mobility group protein (HWG) gene, HWGI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the armshalfon product but not the protein binding domain. These proteins, antibodies derived from these proteins or expression modulators of the HWGI-C protein can be used in kits to modulate vascular development. Such
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                                                                                                                   708 ggcggccgctctagaggatccaagcttacgtacgcgtgcatgcgacgtcatagctcttct 767
                                                                                 Gaps
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Why: 97-33887/31.
DNA sequences representing aberrant forms of human high mobility
group protein genes - useful for treatment of endometriosis and
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                                   Score 71; DB 38; Length 533;
Pred. No. 2.80e-26;
0; Mismatches 1; Indels
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                                                                               1; Indels
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  127 G;
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  146 C;
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V02883 standard; cDNA; 774 BP.
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Human HMGI-C aberrant form 19.
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Juman HMGI-C aberrant form 4.
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    Ä
                                     7.1%;
larity 98.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue regeneration; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1995; DE-048122. (BULL/) BULLERDIEK J.
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21-DEC-1995; 048122.
21-DEC-1995; DE-0481
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BP;
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nes 72; Conser
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DE19548122-A1.
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Matches
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but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MK14-A consists of nucleotides 5-95 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
051746 standard; cDNA; 91 BP.
051746;
31-MAY-1994 (first entry)
Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
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Local Similarity 12.7%; Pred. No. 3.27e-10;
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06-JUN-1996; U09306
                                                                         204 BP;
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19-DEC-1996.
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Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T; WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.coli ferracious were introduced into the alpha fragment of stander galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for
                                                                                                                                                                                                                                                                                                                            claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CS05135). It hybridized to all spp. of mycobacteria tested, but
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                        New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; p; English.
Random point mutations were introduced into the alpha fragment
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                                                                                                                                                  Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
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187..204
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0.0%; Pred. No. 1.14e-09;
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                                                                                                              standard; cDNA; 91 BP.
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                                                                                                                                     31-MAY-1994 (first entry)
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                  Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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WPI; 93-378844/48
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                                                            427 TTC 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-285123-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1988
                                                                                                                                                                                       Synthetic
                                   ctc
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                    samples
                                                                                                            051746
                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                               RESULT
ID OF
AC OF
DE OI
DE OI
NW SE
NW SE
PD OI
PP OI
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ID N8
AC N8
DT 08
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonuclectide (ON) to the airway epithalium of the subject. The present sequence is an antisense oligonuclectide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antišense ON its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; O A; 52 C; 46 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                     76 ycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddh 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 ccttggcbbgccbcbbbcbgcbgbgbbbbtcbtgbgcbbbtbbtccbttctgbbbbbb 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TCCCAAGCAGGAGGCGCCCAAGGGCCGCACCCGGGACCCCGGTGGGGCGCTGACCCAGGC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 yvybbbv-ynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvc 189
                                                                                                                                                                                                                    108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 TGAGCGCGCACAGCGCCCAGGCCGCACAGGGCCCCGAAACGCCCCATCGCCCC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human endothelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                     57; Mismatches 40; Indels
                                                                                                                                                                                                                        11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 32;
Pred. No. 3.97e-09;
                                                                                                                                                                                                                                                                                                                      Pred. No. 1.14e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 32;
                                                                                                                                                                                                                    17 G;
                                                                                                                                                                                                                 47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 38; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N81164 standard; DNA; 204 BP
N81164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, Nyce JW;
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.1%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                        4.28;
                                                                                                                                                                                                                    21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 11
T76405 standard; DNA; 178
T76405;
                                                                                                                                                                                                                                                                                                                                                        17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 bgggbtcbbbbbc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 cceedraceccc 107
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Query Match
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8888888888
                                                                                                                                                                       Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,
mishlocorporation, completion of molecules and screening.

Disclosure; p; English.

English matations were introduced into the alpha fragment of
Random point mutations were introduced into the alpha fragment of
E. coli beta galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which
see also P80575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 265-266; 433pp; English.

Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (FTM) BN enzyme. Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae Radi/RadiO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are compared to the clavage products of reference gene sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pGEM32f target fragment.
p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
Staphylococcus; identification; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                    17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaa 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fors L, Heisler LM, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Length 204;
Pred. No. 4.69e-08;
27; Mismatches 7; Indels
                                      /function=multiple cloning site
187..204
/*tag= b
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Location/Qualifiers
19..69
                                                                                                                                                                                                                                                                                                                                                                                                  47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 13
T27694 standard; DNA; 206 BP.
                                                                                                                                                                                                                                                                                                                                                                                                  21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                               3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 33.3%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1996 (first entry)
                              ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahlberg JE,
MC, Olive DM;
                                                                                                                                      (SUSO) SUOMEN SOKERI OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1994; US-337164.
09-MAR-1995; US-402601.
07-JUN-1995; US-484956.
30-AUG-1995; US-520946.
                                                                                                                         US-034819
                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1996.
09-NOV-1995; U14673.
                                                                                                                                                                                                                                                                                                                                                                                                     204 BP;
                                                                                                           30-MAR-1988; 105163
                                                                                                                                                  Lehtovaara P, Knowl
WPI, 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 96-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
W09615267-A1.
 Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oldenburg MC
                                                      primer_bind
                                                                                 EP-285123-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ID T2
AC T2
DT 02
DE PG
KW P5
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identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter.
Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococus. The method may also be used for the identification of viruses, especially hepatitis C virus and similan immunodeficiency virus. Fragments of the vector pGEM32f were used as a test sequence for the method. The fragments were used alongside test fragments of the
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays Example 1C; Fig 21; 93pp; English. The ability of 5' nucleases derived from thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
Disclosure; Fig. 21; 159pp; English.
The ability of 5' nucleases derived from thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA SUBSTRATE (or 5, nuclease.
DNA polymerase; 5' nuclease activity; DNA cleavage; RNA cleavage;
transcleavage; hairpin structure; ss.
                                                                                                                                                                                                                                                                                                            ö
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0
                                                                                                                                                                                                                                                       Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-polymerase; DNAP; 5' nuclease; Thermus; DNA cleavage;
RNA cleavage; transcleavage; hairpin; ds.
                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-polymerases to cleave a specific sequence structure was tested using the present duplex sequence, and the pilot oligonucleotides given in T70337-39. Sequence 206 BP. 49 A; 48 C. 52 G; 57 T;
                                                                                                                                                                                                          57 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1006 TITCCCAGICAGGACGIIGIAAAACGACGGCCAGIGAATIG 966
                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                    4.69e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 37; I
Pred. No. 4.69e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                           10 tttcccagtcacgacgttgtaaaacgacggccagtgaattg
                                                                                                                                                                                                          52 G;
                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                                                       Score 39; DB 23
Pred. No. 4.69e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO942;
22-DEC-1994.
06-JUN-1994; UG6253.
04-JUN-1993; US-073384.
A (THIR-) THIRD WAYE TECHNOLOGIES INC.
A "THIR-) THIRD WAYE TECHNOLOGIES INC.
A "THIR-) THIRD WAYE TECHNOLOGIES INC.
                                                                                                                                                                                                          48 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (THIR-) THIRD WAVE TECHNOLOGIES INC.
Brow MAD, Dahlberg JE, Lyamichev VI;
WPI; 97-201481/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.9%;
Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                          49 A;
                                                                                                                                                                                                                                                     3.9%;
Local Similarity 97.6%;
les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1995 (first entry) 5' Nuclease substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T70340;
03-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 15
Q80775 standard; DNA; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T70340 standard; DNA; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
US5614402-A.
25-MAR-1997.
06-JUN-1994; 254359.
07-DEC-1992; US-986330.
04-JUN-1993; US-073384.
                                                                                                                                                                             human tyrosinase gene.
Sequence 206 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
WO9429482-A.
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DNN-polymerases to cleave a specific sequence structure was tested using the duplex sequence given in 080775 and the pilot oligonucleotides given in 080758-60. Sequence 228 BP; 59 A; 56 C; 53 G; 60 T;
88888
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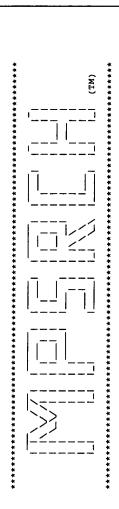
Query Match

3.9%; Score 39; DB 13; Length 228;
Best Local Similarity 97.6%; Pred. No. 4.69e-08;
Matches 40; Conservative 0; Mismatches 1; Indels

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0; Gaps

Search completed: Fri May 14 08:09:48 1999 Job time : 166 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Fri May 14 07:16:35 1999; MasPar time 1611.89 Seconds 1474.893 Million cell updates/sec :uo

>US-08-911-423-3 (1-1006) from US08911423.seq 1006 abular output not generated. Description: Perfect Score: N.A. Sequence: Comp: Title:

1 ATGGCACAGCAGCGGGCGAT.....ACAACGTCCTGACTGGGAAA 1006 TACCGTGTCGTGCCCCGCTA.....TGTTGCAGGACTGACGTTT TABLE default Gap 6 Scoring table:

602357 segs, 1181590623 bases x 2 Dbase 0; Query 0 Searched:

••

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_vi Database:

16:9b_bai 17:9b_ba2 18:9b_htg 19:9b_in 20:9b_om 21:9b_ov 22:9b_pat 23:9b_ph 24:9b_pli 25:9b_pi2 26:9b_pri 27:9b_pri 28:9b_pri Database:

Mean 10.691; Variance 5.553; scale 1.925 tistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	2.358-151	1.95e-63	7.72e-56	3.80e-40	6.09e-38	3.04e-29	8.14e-28	2.80e-24	1.74e-21	8.55e-21	4.19e-20	2.04e-19	9.85e-19
	Description	Mus musculus glucocort	Cloning vector pSport1	Cloning vector pSport2	Sequence 1 from patent	Saccharomyces cerevisi	HIV-1 strain MO2 from	Human HepG2 3' region	Sequence 1 from patent	human STS SHGC-2867 cl	LSCV119 Caprine BAC Ca	Cloning vector pSySpor	Cucumis sativus mRNA f	human STS SHGC-6182 cl
SUMMARIES	ΩI	MMU82534	PSPORT1	XXU12391	160018	SCU15970	HIVU84854	HUMD4H12M3	AR023813	G13951	G41212	PSVSPORT	CSPATATLP	G14155
	igth DB	1020 29	4109 33	4310 33	581 22	5772 24	2699 34	98 27	538 22	398 31	433 31	3160 32	1297 24	414 31
	% Query Match Length DB		`	10.5	8.4		7.0	8.9	6.3	5.9	5.8	5.7	5.6	5.5
	Score N	228	116	106	82	82	20	68	63	29	28	57	26	22
	Result No.	-	c 5	3 G	4	Ω	و د	7	00	σ	10	11	12	13

9.85 4.745 4
Cloning vector pGEM-42 human STS SHGC-3196 cl sequence 14 from patent Scyvil6 Caprine BAC Ca Sequence 14 from patent Cryptosporidium parvum pBluescript KS(+) vect pBluescript KS(+) vect pBluescript KS(+) vect pBluescript KS(+) vect cloning vector pGEM-11 cloning vector pBB prividus gene for 18 pExcell cloning vector pBB cloning vector pBC caenorhabditis elegans human DNA for Ig gamma **** SEQUENCING IN PROG caenorhabditis elegans ****
CUPGEM42 G16894 G16894 G17976 G17976 G17976 G17976 G17976 G1210 G41210 G
188 188 188 188 188 188 188 188
2746 390 4103 1359 965 2185 216 2288 2988 2988 2988 2988 2988 3123 323 323 4409 4109 4139 4439 4439 4439 4439 4439 4439 443
$\begin{matrix} \mathbf{n}_{N}\mathbf{n}_{A}\mathbf{a}_{A}\mathbf{a}_{A}\mathbf{a}_{A}\mathbf{a}_{A}\mathbf{a}_{A}\mathbf{n}_{B}\mathbf{n}_{\mathsf$
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40011011010000000000000000000000000000
0 00 00000 0000 0 0

ALIGNMENTS

	MNO82534 IUZU DP MRNA ROD IB-OCT-199/		U82534	q2228583		house mouse.		Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	Rodentia; Sciuroquathi; Muridae; Murinae; Mus.	1 (bases 1 to 1020)	Nocentini, G., Giunchi, L., Ronchetti, S., Krausz, L.T., Bartoli, A.,	Moraca, R., Migliorati, G. and Riccardi, C.	A new member of the tumor necrosis factor/nerve growth factor	receptor family inhibits T cell receptor-induced apoptosis	Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6216-6221 (1997)	97322352	2 (bases 1 to 1020)	Nocentini, G., Giunchi, L., Ronchetti S., Krausz, L.T., Bartoli, A.,	Moraca, R., Migliorati, G. and Riccardi, C.	Direct Submission	Submitted (18-DEC-1996) Carlo Riccardi, Clinical Medicine,	Pathology and Pharmacology, Perugia University, V. del Giochetto,	Perugia, PG 06100, Italy	Location/Qualifiers	•	/organism="Mus musculus"	/strain="C3H/HeN"	/db_xref="taxon:10090"	/cell_type="thymocytes"	46732	/note="type I transmembrane protein; belongs to the tumor	mecrosis ractor receptor/merve growth ractor receptor family"	/codon start=1	
RESULT	DEFINITION	1071717	ACCESSION	OIN	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS		TITLE		JOURNAL	MEDLINE	REFERENCE	AUTHORS		TITLE	JOURNAL			FEATURES	sonrce					CDS				

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misc_feature
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KEYWORDS
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                                                                                  TITLE
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                                                                   MAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTE
EKCHLGGRWP"
           /db_xref="PID:9228584"

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CSLYAPGKEDCPKERCYMTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 CAGGCCAGGGGGTACAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTG 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                               167 GCTGCTGCCGCGATTACCCGGGCGAGGGTGCTGTTCCGAGTGGGACTGCATGTGTGTCC 226
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                                                                                                            103. .729
/note="type I transmembrane protein"
/product="glucocorticoid induced TNFR family
                                                                                                                                                                                                                                                                                                                                                                                        Length 1020;
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Pred. No. 2.35e-151;
0; Mismatches 144; Indels
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/note="encodes TNFR cystein repeat 1"
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                                                                                                                                                                                                                                                                                       505. .573
/note="encodes transmembrane domain"
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/note="encodes extracellular domain"
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/note="encodes
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Best Local Similarity 72.1%;
Matches 372; Conservative
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23-AUG-1994

UNA

Cloning vector pSportl, complete cds. U12390 9531828

DEFINITION ACCESSION NID

4109 bp

PSPORT1

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/evidence=experimental
/product="lac repressor"
/d_xref="plD:g531830"
/translation="kRPVTLEVDABYAGVSYQTVSRVVNQASHVSAKTREKVBAAMAE
LNYIPNRVAQQLAGKQSLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILESFRPBERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"beta-galactosidase alpha peptide"
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/translation="WMITPSSWTHTHYRESWYACRYRSGIPGSTSSLVGGRSRGSKLT
YACMRRHSSSIVSPKFNSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVEACKAAVHNILAQRVSGLIINY PLDDQDAIAVEAACTNVPALFLDVSDQTPINSII
FSHBOGTRLOVBHLYALGOQIALLAGPLSSVSARLRIAGAHKYLTRNOIQPIAEREG
PSSSCYIPPSTTIKQDFRLLGQTSVVDRLLQLSGGAKAUTESCLRVGADISVVSYDDT
BDSSCYIPPSTTIKQDFRLLGQTSVVDRLLQLSGGAVKGNQLLPVSLVKRYTTLAPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="Escherichia coli"
complement(125. 147)
/standard_name="M13/pUC 23 base forward sequencing primer"
                                                                                              1 (sites)
D'Alessio,J.M., Gruber,C.E., Cain,C. and Noon,M.C.
Construction of Directional cDNA Libraries Using the Superscript
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/standard_name="CRLE; coli pMB1 (ColE1 and pBR322)"
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/standard_name="M13/puc forward sequencing primer"
/evidence-experimental
164. 180
                                                                                                                                                                                                                                                                                                               Submitted (18-JUL-1994) Horton M. E., Life Technologies, In
Technical Services, 8400 Helgerman Court, Gaithersburg, MD
20884-9980, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Cloning vector pSportl"
/db_xref="taxon:36586"
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                                                                 artificial sequence; cloning vectors
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/db_xref="PID:9531831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /plasmid="pSport1"
/db_xref="taxon:32644"
/lab_host="Escherichia
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191. .285
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1. .4109
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Cloning vector psportl. Cloning vector psportl
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2 (bases 1 to 4109)
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Direct Submission
                                                                                                                                            Construction of
Plasmid System
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Unclassified.
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Matches 108; Conser
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                DRWEPELNEAIPUDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence-experimental
/product-"beta-galactosidase alpha peptide"
/dzxref-"plD:g825756
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TYACMRRHSSSIVSPKFNSLAVVLORRDWENPGVTQLNRLAAHPPFASWRNSEBARTD
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (sites)
Gruber, C.E., Li, W., Lin, J. and D'Alessio, J.M.
Subtractive cDNA hybridization using the multifunctional plasmid
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Submitted (18-JUL-1994) Mary E. Horton, Life Technologies, Inc.,
Technical Services, 8400 Helgerman Court, Gaithersburg, MD
                                                                                                                                                                                                                                      122 TITCCCAGICA¢GACGIIGTAAAACGACGGCCAGIGAATIIGAAITIAGGIGACACIAIAG 181
                                                                                                                                                                                                                                                                                     AGAGCGGCCGCCGA 241
                                                                                                                                                                                                                                                                                                     24-MAY-1995
                                                                                                                                                                                           Gaps
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/note="M13/pUC 23 base forward sequencing primer"
complement(150. .161)
/note="M13/pUC forward sequencing primer"
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                                                                                                                                                            Length 4109;
                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                   182 AAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTTGGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Cloning vector pSport2"
/plasmid-"pSport2"
/db.xref-"taxon:36587"
/lab_host-"Escherichia coli"
complement(<1 .344)
                                                                                                                                                                                                                                                                                                                                                                      XXU12391 4310 bp DNA UNO CLONING Vector pSport2, complete sequence. U12391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="multiple cloning site"
                                                                                                                                                         Score 116; DB 33;
Pred. No. 1.95e-63;
0; Mismatches 2;
                                                            3667. .4109 /note="F1 intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector pSport2 artificial sequence; cloning vectors.
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/note="T7 promoter"
/evidence=experimental
complement(467. .1549)
                                                                                           /evidence=experimental
1064 c 1062 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector pSport2
Focus 15 (3), 59-65 (1993)
2 (bases 1 to 4310)
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/transl_table=11
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                                                                                                                                                         11.5%;
ilarity 98.3%;
Conservative
                                               EIGASLIKHW"
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                                                                                                                                                                         Similarity
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Best Local :
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KEYWORDS
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LOCUS
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/evidence=experimental
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/d_xxef="PID: 95318X4
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LNYIPNRVAQQLAGKQSLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERS
                                                                                                                                                                             FSHEDGTRLGVEHLVALGHQO1ALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREG
DWSAMSGFQQTWQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDT
EDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IELDLNSGKILESFRPEERFPMASTFKVLLCGAVLSRIDAGQEOLGRRIHYSONDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTWPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
                                                                                                                                                         GVEACKAAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRSALPAGWF1ADKSGAGERGSRG11AALGPDGKPSR1VV1YTTGSQATMDERNRQ1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 TTTCCCAGTCACGACGTTGTAAAACGACGCCCAGTGAATTGAATTTAGGTGACACTATAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1896. .1902)
/standard_name="ORI E. coli pMB1 (ColE1 and pBR322)"
/evidence=experimental
complement(2706. .3566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-1997
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/transl_except=(pos:complement(1547. .1549), aa:Met)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1581;
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1. No. 3.80e-40;
Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/function="ampicillin resistance"
/puidence=experimental
/product='beta-lactamase"
/db_xref="PID:9531835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 106; DB 33; I
Pred. No. 7.72e-56;
0; Mismatches 2;
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Patent: US 5654495-A 1 05-AUG-1997;
Location/Qualifiers
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3667. .4109
/note="F1 intergenic region"
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                                                                                                                                                                                                                                               OTASPRALADSLMOLAROVSRLESGO"
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Voelker,T.Alois and Davies,H.Maelor.
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160018
92478650
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
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356 c 410 g
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                         /transl_table=11
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98.2%;
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Best Local Similarity 98.9%;
Matches 86; Conservative
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DEFINITION

ACCESSION

SOURCE ORGANISM

KEYWORDS

RENCE HORS

JOURNAL MEDLINE AUTHORS JOURNAL

REFERENCE

TITLE

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lentivirus group.

1 (bases I to 2699)

Connor, R. I., Korber, B. T. M., Graham, B. S., Hahn, B. H., Ho, D. D.,
Walker, B. D., Neumann, A. U., Vermund, S. H., Mestecky, J., Jackson, S.,
Fenamore, E., Cao, Y., Gao, F., Kalams, S., Kunstman, K. J., McDonald, D.,
McWilliams, M., Trkola, A., Moore, J. P. and Wolinsky, S. M.
Immunological and virological analyses of persons infected by human immunodeficiancy virus type 1 while participating in trials of
Trecombinant gpl20 subunit vaccines
J. Virol. 72 (2), 1552-1576 (1998)
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HTDNNTEIFREGGEDMRDNWRSELKYKVWIEPLGYAPTKARRKVOREKRAVGIGA
MFLGFLGAAGSTWGAASVTULVGARLLLSGIVQQOSNLLRAIEAQOHLLQUTVWGIRC
LQARVLSVERYLKOQQLGIWGCSGKLICTTTVPWNASWSNKSLNAIWDNTTWWGIRC
LSNYTVLKYSIIESONOQEKNELELLELDKWASLANWFDITNWLWYIKIIENVIGG
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DGFLALIWDDLRSLCLESTHRRDLLIVELLGROFFRKWGNLIQYMIQELKKSA
ISLLNATAIVVABGTDRAIEALQYBGRAILHIPRRIRQGLERALL"
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ARGFRALIKCNNKTFSGKGPCTNVSYVGCTHGITRYVSTGLICHGSLEKEKETITSDD
FSDNTKTITVQLNESVAIDCIRPSNNTRKSTHIGPGRAFYATGITIGDIRQAHGTINR
TQWNQTLDRVIRKLKQFVNKEIEFKGSSGGDPEIVMHSVNGGEFFYCNTTQLFNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:11676"
/note="subtype B; PBMC from an early vaccine-break control
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/db_xref="PID:g2290121"
/translation="MRVKGIRKNYQHWWWRWGMMLLGMLMISSATEKLWVTVYYGVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WKEATTTLECASDAKAYDTERHNVWATHACVPTDPNDGEVLLENVTENFNWKNNMVE
QMHEDIISLWDQSLKPCVKLTPLCVTLNCTDVTLNSTGVNVTNELKNLTNEMKNCSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JAN-1997) HIV Database, Los Alamos Nat'l Labs, Mail Stop K710, Los Alamos, NM 87545, USA Location/Qualifiers
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/organism="Human immunodeficiency virus type
/proviral
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/db_xref="PID:92290122"
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                                                                                                           Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
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Wolinsky, S. and Hahn, B.
Direct Submission
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/gene="nef"
2663. .>2699
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/gene="env"
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/gene="env"
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Best Local Similarity 98.6%;
Matches 71; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (13-OCT-1994) Nathan Nelson, Roche Institute of Molecular
Biology, 340 Kingsland St., Nutley, NJ 07110, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYISIVWILWLGLISYYESVVVKRAMKKQWSTWEDWPEGAESHRVGLFADPQIMDEY
SYPGRPQIVNYFTRVIVDHYHRRNWKYVQYYLDPDSNFFLGDLFDGGRNWDDKQWIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTRFNQİFPKKPLRRTVMSLPGNHDIGFĞDTVVESSLQRFSSYFGETSSSLDAĞNHTF
VLDTISLSDKTNPNYSRVPRQFLDNRAMGSHPLPRLILTHYPLMRDPEQQTGGQLRE
SKEPPF JOKGHQYQTVIENDISQELITKIQPEILFSGDDHDHCQISHSYPFGGKTKNA
QEITYKSCAMMMGISRAJQLLSLYNPSDLIMVNAGGEYASKTYQTELCYMPDYKAI
RMYLMGLLFSAAFIAYMHFFPKSFNNRVATIMNRVFTRPDGNTSDLPLFISISKSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVYRNRSKSVLSTHSKKSDDKAHYKSRSKKKSKSRSKKRLRIYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CDC1; similar to S. cerevisiae CDC1 gene product, encoded by GenBank Accession Number X81813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Dases 1 to 5772)
Supek,F., Supekova,L., Nelson,H. and Nelson,N.
A yeast manganese transporter related to the macrophage protein involved in conferring resistance to mycobacteria
Proc. Natl. Acad. Sci. U.S.A. 93 (10), 5105-5110 (1996)
889 GGCGCCGCTCTAAAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900 TAAAGGAICCAAGCITACGIACGCGIGCAIGCGACGICAIAGCICIICIAIAGIGICACC 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1998
                                                                                                                                                                                                                   18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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DEFINITION HIV-1 strain MO2 from USA, envelope glycoprotein (env) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5642 TACAAGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCTATAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotaė; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSLTHSKYAVNDTRSIKQFLVNAIVLEVSVMPIFIYFYTVV"
1015 c 1053 g 1875 t
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                                                                                                                                                                                                                                    Saccharomyces cerevisiae CSP2 gene, complete cds. U15970

    5772
/organism="Saccharomyces cerevisiae"
/strain="W303"

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Pred. No. 6.09e-38;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SGD:L0000241"
2462. .3937
/gene="CSP2"
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/db_xref="SGD:L0000241"
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2462. .3937
/gene="CSP2"
                                                    1555 ATAGTGTCACCTAAATTCAATTCACTG 1581
                                                                            949 ATAGTGTCACCTAAATTCAATTCACTG 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'function="unknown"
                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
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Nelson, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.2%;
Best Local Similarity 90.7%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                               baker's yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces.
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96209864
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61 AGAGCGGCCGCC 72

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RESULT

BASE COUNT ORIGIN

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DEFINITION

RESULT

ACCESSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

URNAL ERENCE

AUTHORS TITLE

JOURNAL

COMMENT

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 2 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue
                                                                                                                                                                                                                                441 GCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATNN-TCTTCTT 499
                                                                                                                                                                                                                                                                      890 GCGCCCCTCTAAAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCTA 949
                                                                                                                                                                                     2; Gaps
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62 degrees C for 23 seconds
72 degrees C for 30 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                           Length 538;
                                                                                                                                           Score 63; DB 22; Length 538
Pred. No. 2.80e-24;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                   Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                      SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91129690
STS sequence; primer; sequence tagged site.
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Location/Qualifiers
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0.05 units/ul
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  Patent: US 5795740-A 1 18-AUG-1998;
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each 1 uM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    G13951 398 bp DNA
human STS SHGC-2867 clone pG-564
G13951
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50 mM
20 mM
8.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ul
                                                           /organism="unknown"
123 c 137 g
                       Location/Qualifiers
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Polymerization:
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Taq Polymerase:
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                                                                                                                                             Query Match 6.3%;
Best Local Similarity 86.5%;
Matches 83; Conservative
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PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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  JOURNAL
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ORGANISM
                                                                                  BASE COUNT
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JOURNAL
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                       FEATURES
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                                                                                                       ORIGIN
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The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
94357437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Matoba, Osaka University, Institute for Molecular and Cellular Bio;
1-3, Yamada-oka, Suita, Osaka 565, Japan
(E-mail:matoba@inherit.imcb.osaka-u.ac.jp,
Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
Submitted (21-Jul-1993) to DDBJ by:
                                                                                                                                                                                       gene signature.
Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
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                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2 Kizugawadai Kizu-Cyo,
Kizugawadai Kizu-Cyo,
Soraku-gun, Kyoto
Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GCGGCCGCTCTAGAGGATCCAAGCTTACGGACGCGTGCATGCGACGTCATAGCTCTTCTA 68
                                                                                                       01-DEC-1994
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Platica,M., Platica,O. and Holland,J.F.
Pituitary differentiation factor and methods of use thereof
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                                                                                    HUMD4H12M3 98 bp mRNA PRI
Human HepG2 3' region MboI cDNA, clone hmd4h12m3.
D17247
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR023813 538 bp DNA Sequence 1 from patent US 5795740.
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est Local Similarity 87.6%;
latches 78; Conservative
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900 AGAGCGCCGCC 889
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source

FEATURES

BASE COUNT

ORIGIN

Matches

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RESULT LOCUS

DEFINITION

ACCESSION NID KEYWORDS ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

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/evidence-experimental
/product="beta-lactamase"
/d_xref="plis-g540253"
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IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                             /strain="Saanen"
/note="Vector: pBeloBAC11; V-type: BAC; Genomic HindIII
fragments (average size 150 kb)"
/db_xref="taxon:9925"
/clone_lib="Caprine BAC"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 TTCTATAGTGTCACCTAAATCCAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGA 351
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-SEP-1994) Mary E. Horton, Life Technologies, Technical Services, 8400 Helgerman Court, Gaithersburg, MD
                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 31; Length 433;
Pred. No. 8.55e-21;
0; Mismatches 2; Indels

    .3160
    /organism="Cloning vector pSvSportl"
/db_xref="taxon:40160"

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Cloning vector pSVSport1
artificial sequence; cloning vectors.
                                                                                                                                                                                                                                                                                                                    83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Life Technologies, Inc. Catalogue Unpublished (1994)
C (1988)
Horton, M.E.
Direct Submission
                                                              /organism="Capra hircus"
                                                                                                                                                                                  /tissue_type="skin"
/cell_type="fibroblast"
/cell_line="CAT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2003. .2863)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                               complement(206.
         Chromosome localization
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Best Local Similarity 96.8%;
Matches 60; Conservative
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D'Alessio,J.M.
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polyA_signal
rep_origin
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                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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NID
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                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Teres 1 to 433)
Vaiman,D., Schibler,L., Oustry-Vaiman,A., Pailhoux,E., Furet,J.-P., Goldammer,T., Cotinot,C., Schwerin,M., Fellous,M. and Cribiu,E.P. High-resolution human/goat comparative map of the goat Polled/Intersex Syndrome (PIS): The human homologue is contained in Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                       G41212 433 bp DNA STS 19-AUG-1998
LSCV119 Caprine BAC Capra hircus STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratoire de Genetique biochimique et de Cytogenetique
Institut National de la Recherche Agronomique
Centre de Recherche INRA de Jouy-en-Josas, 78352 Jouy-en-Josas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer: each 1 uM
dGTP, dCTP, dTTP: 100mM, dATP: 10mM + alpha P33 dATP 0.5 uCi
Taq Polymerase: 0.05 units/ul
                                                                                                                                                                                                                      320 GGCGGNCNCTCTAGAGGATCCAAGCTTACGTACGCGTGCAINCGANGTCATAG-TCTTCT 378
                                                                                                                                                                                                                                           goat.
Capra hircus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                                                                        Gaps
                                                                                                                                                  Score 59; DB 31; Length 398;
Pred. No. 1.74e-21;
0; Mismatches 8; Indels
                                                                                               10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denaturation: 94 oc for 15 seconds
Annealing: 58 oc for 20 seconds
Polymerization: 72 oc for 20 seconds
PCR cycles: 30
Thermal cycler: MJ Research or Perkin-Elmer Cetus
Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 33134652672
Fax: 33134652478
Email: cribiu@biotec.jouy.inra.fr
Primer A: CAAGCTACAGTCTATAGGGTC
Primer B: CTACACTGGCCAGAGGATTC
STS size: 155
PCR Profile:
                      /organism="Homo sapiens
                                       110. .241
110. .132
complement(219. .241)
a 83 c 100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presoak: 94 oC for 5 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Edmond P. Cribiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Template: 30-100 ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MH4)2SO4: 20mM
Tween20: 0.01% w/v
Tris-HCl: 75 mM
                                                                                                                                                Query Match 5.9%;
Best Local Similarity 88.2%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                              379 NTNGTGTCAACTAAAT 394
                                                                                                                                                                                                                                                                                                                  949 ATAGTGTCACCTAAAT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MgC12: 2 mM
                                                                                              101 a
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g3435060
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                                                          primer_bind
                                                                         primer_bind
BASE COUNT
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     source
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ORGANISM
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COMMENT
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TITLE

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BASE COUNT

12

RESULT

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DEFINITION

ORGANISM

WORDS

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE AUTHORS JOURNAL

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Ctarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 15 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 GGCGGCCGTTCTNGAGGATCCAAGCTTACGTACGCGTGCATGCGACGNCATAGGCTCTNC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seconds
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                                                                                                                                                                                                                                               Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 31; Length 414
Pred. No. 9.85e-19;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
23
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degrees C for 1
degrees C for 2
degrees C for 3
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                                      STS sequence; primer; sequence tagged site.
human.
Homo sapiens
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0.05 units/ul
10 ul
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each 1 uM
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76. .196
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72
30
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87 g
                                                                                                                                                                                                                                                                                                                                                              Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                     Primer A: TCCCACAACAGTAAAGGAG Primer B: CAAGGTATGGTGACGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쥩쥩줱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for Medical Research, Camden,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
20
8.3
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Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.5%;
Best Local Similarity 87.2%;
Matches 82; Conservative
                                                                                                                                                                                                            Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annealing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rotal Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    remplate:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MgC12:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STS size: 121
PCR Profile:
                                                                                                                                                                                             Myers, R.M.
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                     g1129894
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   ACCESSION
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                                      KEYWORDS
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ORIGIN
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWPPELNBAIPNDREDTTMPVAMATTLRKLLTGELLTLASRQOLIDWMEADRVAGPL
EIRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW" 775 c 724 g 841 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:92462265"
//db_xref="PID:92462265"
//translation="PRVRFLSLFVLLTMVADFAKGKMITILSIDGGGIRGIIPSIILA
FLESKLQELDGPDVRIADYFDVIAGTSTGGLVTSMLTAPDKNNRPLYSASDLALFYIE
HAPKIFPQRNYFLCSLVNFFGKVMGFKYNGLYLKSLIKGLLGDITLKQTLSQVVIPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIKLLOPVIFTTIEAKCSELKNPKLADVCISTSAAPTFLPGYEFQTKDSKGNIRNYEM
VOGYVANNPPLAAMTHVYKEMSILIRHRSELLKIKPMETERMLVLSLGTGTPKNDEKY
SAARASKWGMLDWYHGGGTPIVDIFSDASADMVDYHISSIFQSDHCHKNYLRIQDDT
LSGEVSSVDIATEBNLLNLIYYGENLLKKPLSRVNLESGKFEPLDARGTNBQALABFA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuccumis sativus

Cuccumis sativus

Eukaryoteae, Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; vascular plants; seed plants; Magnoliophyta;

Magnoliopsida; Violales; Cucurbitaceae; Cucumis.

1 (bases 1 to 1297)

1 (bases 1 to 1297)

1 the partain-like protein localized to lipid bodies involved in the mobilization of fat reserves?
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-APR-1997) H. Kindl, FB Chemie Universitaet Marburg,
Hans-Meerwein-Strasse, 35043 Marburg, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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/function="mobilization of fat during seed germination"
                                                                                                                                                                                                                                                                                                            CSPATATLP 1297 bp RNA PLN 30-SEP-1997
Cucumis sativus mRNA for patatin-like protein, partial.
Y12793
                                                                                                                                                                                                                                416 TCGGCGCCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGCCCCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTT 1297
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                                                                                                                                Score 57; DB 32; Length 3160;
Pred. No. 4.19e-20;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="patatin-like protein"
/db_xref="PID:e316871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 24; I
Pred. No. 2.04e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Cucumis sativus"
/db_xref="taxon:3659"
/tissue_type="cotyledon"
/clone_lib="psporr"
/clone="cshsp70291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS G14155 414 bp DNA
DEFINITION human STS SHGC-6182 clone pg-2782.
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Local Similarity 98.3%;
les 57; Conservative
                                                                                                                                Query Match 5.7%;
Best Local Similarity 98.3%;
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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source

FEATURES

TITLE

CDS

Gaps

Query Match

Matches

1240

BASE COUNT ORIGIN

13

RESULT

948

05-MAR-1996

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DEFINITION ACCESSION

KEYWORDS

SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

IN

REMARK

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniotae; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                      STS sequence; primer; sequence tagged site.

human Plasmid clones, generated from a lymphoblastoid cell line
Localized to human chromosome 5 by analysis on
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1006 TITCCCAGTCAGGACGTTGTAAAACGACGCCCAGTGAATTGAATTTAGGTGACACTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 degrees C for 15 seconds 64 degrees C for 23 seconds 72 degrees C for 30 seconds 30 Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 31; Length 390
Pred. No. 4.74e-18;
0; Mismatches 10; Indels
                                                                                              SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              each 1 uM
each 200 uM
0.05 units/ul
10 ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: TIGITGATGATCTGCGATATGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                 ытовч4 390 bp DNA
human STS SHGC-3196 clone pG-1108.
G16894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer B: GGCCAAAAAAGCGAAGCTCCATC
STS size: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     죝죝죝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  пg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.4%;
Best Local Similarity 85.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annealing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total Vol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dNTPs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MgC12:
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STS size: 13
PCR Profile:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
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                                                                                                              DEFINITION
ACCESSION
                                                                           15
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                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                  NID
KEYWORDS
SOURCE
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                                                                           RESULT
                                                                                                LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELDLNSGKILESFRPEERFPMASTFKVLLCGAVLSRIDAGOEOLGRRIHYSONDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTWPVAMPTTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (28-MAY-1993) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
This vector can be obtained from Promega Corporation, Madison, WI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                         Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2688 TITCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGGATTTAGGTGACACTATA 2746
                                                         gene; cloning vector; lac2 gene; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="SP6 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="T7 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                         In Wisconsin 800-356-9526
Outside U.S. 608-274-4330
See <X65300-X65335> for related vector sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 32; 1 Pred. No. 9.85e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7. .63
/note="multiple cloning sites"
                                                                     cloning site; promoter.
unidentified cloning vector.
unidentified cloning vector
artificial sequence; cloning vectors.
1 (bases 1 to 2746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2563. .2726
/note="lac operon sequence"
2729. .2746
/note="SP6 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96. .325
/note="lac operon sequence"
complement(108. .110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2746,
/organism="Cloning vector"
/plasmid="Plasmid pGEM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Beta-lactamase"
/db_xref="PID:g58208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="lacz"
/note="lacz start codon"
complement(108. 110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1267. .2127)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Order or Technical 800-356-9526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130. .146
/note="lac operator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="T7 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
 Cloning vector pGEM-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="lac2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="bla"
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Best Local Similarity 96.6%;
                                                                                                                                                                                                                                                   ised by [2]
(bases 1 to 2746)
                                                       beta-lactamase; bla
                                                                                                                                                                    Technical, Services.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Conservative
                                                                                                                                                                                                                                               revised by
                                                                                                                                                                                                                                                                                                                                                                                                     information
                                                                                                                                                                                                                                                                                      Klock, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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promoter

gene

gene

source

FEATURES

9

Gaps

9

promoter

BASE COUNT

ORIGIN

Matches

Search completed: Fri May 14 07:43:41 1999 Job time : 1626 secs.